



1600

RAW SEQUENCE LISTING

DATE: 02/08/2002

PATENT APPLICATION: US/09/308,435B

TIME: 10:35:22

Input Set : N:\Crf3\Refhold\I308435B.raw

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1 <110> APPLICANT: Astra Aktiebolag
 2 <120> TITLE OF INVENTION: Vaccine Delivery System and Method of Production
 3 <130> FILE REFERENCE: 1103326-0560
 C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/308,435B
 C--> 5 <141> CURRENT FILING DATE: 1999-04-09
 6 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00582
 7 <151> PRIOR FILING DATE: 1999-04-09
 8 <150> PRIOR APPLICATION NUMBER: SE 9801288-3
 9 <151> PRIOR FILING DATE: 1998-04-14
 10 <160> NUMBER OF SEQ ID NOS: 25
 11 <170> SOFTWARE: PatentIn Ver. 2.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1670
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Helicobacter pylori
 17 <220> FEATURE:
 18 <221> NAME/KEY: CDS
 19 <222> LOCATION: (793)..(1572)
 20 <400> SEQUENCE: 1

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22 agtccaaaaa gtattagaga atgcttagag gcggtttttc cagcgattcc ttattgctgt 120
23 gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180
24 aaacaataag gtaaaaaaat ccactcactc atttgaatga agaaaatcaa cctaaaaatgg 240
25 tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggt cgatcacgca 300
26 tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360
27 aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
28 gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
29 gttttaaact ctatgcgaga gtcaaaactc aagctaaaaa ggcgtagaaa atggaagcgc 540
30 taatgagtgt gagcgtaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600
31 gcatgacaat tagcgtgtgt atgctggaat ataaaagtgg aggcataaag ggggattata 660
32 acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
33 caacaaaagc gtgttggttg cttcggattt gttgttatag aagctaaaaa tattacaatc 780
34 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
35 Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
36 1 5 10
37 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
38 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
39 15 20 25
40 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
41 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
42 30 35 40 45
43 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
44 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu

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45                               50                               55                               60
46  agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
47  Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
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49  aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
50  Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
51                               80                               85                               90
52  caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
53  Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
54                               95                               100                               105
55  tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
56  Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
57  110                               115                               120                               125
58  gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
59  Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
60                               130                               135                               140
61  gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
62  Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
63                               145                               150                               155
64  tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
65  Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
66                               160                               165                               170
67  ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
68  Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
69  175                               180                               185
70  caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
71  Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
72  190                               195                               200                               205
73  gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
74  Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
75  210                               215                               220
76  agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
77  Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
78  225                               230                               235
79  aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
80  Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
81  240                               245                               250
82  tta aaa ggc aaa aga aac cga taaaacaaa taacgcataa gaaaagaacg 1602
83  Leu Lys Gly Lys Arg Asn Arg
84  255                               260
85  cttgaataaa ctgcttaaaa aggggttttt agcgttcttt ttgagcgtgt atttaagggc 1662
86  tgatgatc 1670
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 260
90 <212> TYPE: PRT
91 <213> ORGANISM: Helicobacter pylori
92 <400> SEQUENCE: 2
93  Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
94  1 5 10 15

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96               20                25                30
97   Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
98               35                40                45
99   Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Arg Pro Ala
100              50                55                60
101   Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
102              65                70                75                80
103   Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
104              85                90                95
105   Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
106              100               105               110
107   Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
108              115               120               125
109   Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
110              130               135               140
111   Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
112              145               150               155               160
113   Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
114              165               170               175
115   Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
116              180               185               190
117   Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
118              195               200               205
119   Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
120              210               215               220
121   Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
122              225               230               235               240
123   Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
124              245               250               255
125   Lys Arg Asn Arg
126               260

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128 <210> SEQ ID NO: 3

129 <211> LENGTH: 1670

130 <212> TYPE: DNA

131 <213> ORGANISM: Helicobacter pylori

132 <220> FEATURE:

133 <221> NAME/KEY: CDS

134 <222> LOCATION: (793)..(1572)

135 <400> SEQUENCE: 3

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136   gatcctatcg cgccaaaggt ggtattagga ataagagctt gattattaat ctccctggta 60
137   agtccaaaaa gtattagaga atgcttagag gcggtttttc cagcgattcc ttattgcgtg 120
138   gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgcccc 180
139   aaacaataag gtaaaaaatg ccaactcactc atttgaatga agaaaatcaa cctaaaatgg 240
140   tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
141   tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360
142   aaactgctat tattgctggg attatggggg ctaaaaagac aagcggaactc attcccatgt 420
143   gccatccaat catgctcaat ggggtggata ttgatatitt agaagaaaaa gagacttgta 480
144   gttttaaact ctatgcgaga gtcaaaactc aagctaaaac ggcgtagaa atggaagcgc 540

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145  taatgagtgt gagcgtaggg cttttaacca ttatgacat ggtgaaagcc attgataaga 600
146  gcatgacaat tagcgggtgtg atgctggaat ataaaagtgg aggcataaagt ggggattata 660
147  acgctaaaaa atagaaaaag actgataatc taaagatatt aggtataaat aacattttga 720
148  caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
149  aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
150      Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
151      1 5 10
152  aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
153  Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
154      15 20 25
155  ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
156  Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
157      30 35 40 45
158  cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
159  Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
160      50 55 60
161  agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
162  Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
163      65 70 75
164  aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
165  Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
166      80 85 90
167  caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
168  Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
169      95 100 105
170  tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
171  Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
172      110 115 120 125
173  gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
174  Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
175      130 135 140
176  gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
177  Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
178      145 150 155
179  tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
180  Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
181      160 165 170
182  ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
183  Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
184      175 180 185
185  caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
186  Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
187      190 195 200 205
188  gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
189  Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
190      210 215 220
191  aga gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
192  Arg Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
193      225 230 235

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194   aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa   1551
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197   tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg   1602
198   Leu Lys Gly Lys Arg Asn Arg
199           255           260
200   cttgaataaaa ctgcttaaaa aggggtttttt agcgttcttt ttgagcgtgt atttaagggc 1662
201   tgatgatac   1670
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 260
205 <212> TYPE: PRT
206 <213> ORGANISM: Helicobacter pylori
207 <400> SEQUENCE: 4
208   Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
209           1           5           10           15
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211           20           25           30
212   Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
213           35           40           45
214   Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
215           50           55           60
216   Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
217           65           70           75           80
218   Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
219           85           90           95
220   Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
221           100          105          110
222   Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
223           115          120          125
224   Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
225           130          135          140
226   Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
227           145          150          155          160
228   Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
229           165          170          175
230   Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
231           180          185          190
232   Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
233           195          200          205
234   Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu
235           210          215          220
236   Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
237           225          230          235          240
238   Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
239           245          250          255
240   Lys Arg Asn Arg
241           260
243 <210> SEQ ID NO: 5
244 <211> LENGTH: 60

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\Refhold\I308435B.raw

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L:4 M:270 C: Current Application Number differs, Wrong Format

L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date